

Amendments to the Claims

This listing of claims will replace all prior versions, and listings of claims in the application.

1. (original) A genetic vector for stable transfection and expression of a desired protein within eukaryotic cells comprising:

- (a) distal 5' flanking sequences of a eukaryotic locus;
- (b) proximal 5' regulatory sequences of a eukaryotic locus;
- (c) at least a first insertion site for a first heterologous coding sequence; and
- (d) proximal 3' regulatory sequences effective for transcription termination of a eukaryotic locus;

wherein said sequences are operably joined in order (a)-(d) in a 5' to 3' orientation, with optional linker sequences between adjacent sequences; and
wherein

- (1) said distal 5' flanking sequences comprise a sequence of at least 100 bases having at least 70% identity to a nucleotide sequence found between 20 bp and 100,000 bp 5' of a transcriptional initiation site of a ferritin heavy chain locus; or
- (2) said proximal 5' regulatory sequences comprise a sequence of at least 20 bases having at least 70% identity to a nucleotide sequence found between 1 bp and 10,000 bp 5' of a translational initiation codon of a ferritin heavy chain locus.

2. (original) A genetic vector for stable transfection and expression of a desired protein within eukaryotic cells comprising:

- (a) distal 5' flanking sequences of a eukaryotic locus;
 - (b) proximal 5' regulatory sequences of a eukaryotic locus;
 - (c) at least a first heterologous coding sequence encoding said desired protein;
- and

(d) proximal 3' regulatory sequences effective for transcription termination of a eukaryotic locus;

wherein said sequences are operably joined in order (a)-(d) in a 5' to 3' orientation, with optional linker sequences between adjacent sequences; and

wherein

(1) said distal 5' flanking sequences comprise a sequence of at least 100 bases having at least 70% identity to a nucleotide sequence found between 20 bp and 100,000 bp 5' of a transcriptional initiation site of a ferritin heavy chain locus; or

(2) said proximal 5' regulatory sequences comprise a sequence of at least 20 bases having at least 70% identity to a nucleotide sequence found between 1 bp and 10,000 bp 5' of a translational initiation codon of a ferritin heavy chain locus.

3. (previously presented) A genetic vector as in claim 1 wherein said distal 5' flanking sequences are derived from a ferritin heavy chain locus.

4. (previously presented) A genetic vector as in claim 1 wherein said proximal 5' regulatory sequences are derived from a ferritin heavy chain locus.

5. (previously presented) A genetic vector as in claim 1 wherein said proximal 5' regulatory sequences and said distal 5' flanking sequences are derived from a ferritin heavy chain locus.

6. (previously presented) A genetic vector as in claim 1 wherein said proximal 3' regulatory sequences are derived from a ferritin heavy chain locus.

7. (previously presented) A genetic vector as in claim 1 further comprising distal 3' flanking sequences of a ferritin heavy chain locus.

8. (previously presented) A genetic vector as in claim 1 wherein said insertion site for a heterologous sequences includes at least one restriction endonuclease site.

9. (original) A genetic vector as in claim 8 wherein said insertion site for a heterologous sequence is a polylinker site including at least two restriction endonuclease sites.

10. (previously presented) A genetic vector as in claim 1 wherein said proximal 5' regulatory sequences include a eukaryotic intron sequence.

11. (original) A genetic vector as in claim 10 wherein said eukaryotic intron sequence is derived from intron 1 of a ferritin heavy chain gene.

12. (previously presented) A genetic vector as in claim 1 wherein said proximal 5' regulatory sequences include untranslated exon sequences.

13. (previously presented) A genetic vector as in claim 1 wherein said distal 5' flanking sequences and said proximal 5' regulatory sequences have a total length of between 1,000 and 10,000 bases.

14. (previously presented) A genetic vector as in claim 1 wherein said proximal 3' regulatory sequences and any distal 3' flanking sequences have a total length of between 1,000 and 10,000 bases.

15. (previously presented) A eukaryotic cell transfected with a vector of claim 1.

16. (original) A eukaryotic cell as in claim 15 wherein said vector has stably integrated into a chromosome of said cell.

17. (currently amended) A eukaryotic cell as in claim 15 wherein said vector comprises a first coding sequence at said first insertion site and said first coding sequence is expressed in said cell.

18. (original) A eukaryotic cell comprising

- (a) distal 5' flanking sequences of a eukaryotic locus;
- (b) proximal 5' regulatory sequences of a eukaryotic locus;
- (c) at least a first coding sequence; and
- (d) proximal 3' regulatory sequences effective for transcription termination of a eukaryotic locus;

wherein said sequences are operably joined in order (a)-(d) in a 5' to 3' orientation, with optional linker sequences between adjacent sequences; and
wherein

(1) said distal 5' flanking sequences comprise an exogenous sequence of at least 100 bases having at least 70% identity to a nucleotide sequence found between 20 bp and 100,000 bp 5' of a transcriptional initiation site of a ferritin heavy chain locus; or

(2) said proximal 5' regulatory sequences comprise an exogenous sequence of at least 20 bases having at least 70% identity to a nucleotide sequence found between 1 bp and 10,000 bp 5' of a translational initiation codon of a ferritin heavy chain locus.

19. (original) A eukaryotic cell comprising:
an exogenous 5' distal flanking sequences derived from a ferritin heavy chain
locus operably joined to a coding sequence.

20. (currently amended) A method of producing a desired protein in a
eukaryotic cell comprising:

- (a) providing at least one cell of claim 17 ~~15~~ or a descendent thereof; and
- (b) maintaining said cell in a culture under conditions which permit high
expression of said desired protein; ~~and~~
- ~~(c) isolating said desired protein from said culture.~~

21. (new) The method of claim 20 further comprising:

- (c) isolating said desired protein from said culture.